

TABLE 1 Elemental rate constants of cognate, near-cognate, and noncognate aa-tRNA binding to the A site^{a,b}

Step		Rate constant (s ⁻¹)		
		Cognate	Near-cognate	Noncognate
Initial binding	k_1	110 ^c	110 ^c	60 ^c
	k_{-1}	25	25	25
Codon recognition	k_2	100	100	
	k_{-2}	0.2	17	
GTPase activation and GTP hydrolysis ^d	k_3	500	50	0.005
GTP-GDP conf. change of EF-Tu	k_4	60	70	
Accommodation of aa-tRNA and formation of peptide bond ^d	k_5	7	0.1	
Dissociation of EF-Tu	k_6	3	2	
Rejection of aa-tRNA	k_7	<0.3	6	

^aData are from References 21–23.

^bKinetic steps and rate constants are defined in Figure 1. Poly(U)-programmed ribosomes were used with ternary complexes of Phe-tRNA^{Phe} (cognate), Leu-tRNA^{Leu2} (GAG) (near-cognate), or poly(A)-programmed ribosomes with Phe-tRNA^{Phe} (noncognate). Rate constants that determine the discrimination are in bold type.

^c $\mu\text{M}^{-1} \text{s}^{-1}$.

^dGrouped for the analysis, because the former reaction is rate limiting.

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22. Rodnina MV, Pape T, Fricke R, Kuhn L, Wintermeyer W. *Initial binding of the elongation factor Tu.GTP.aminoacyl-tRNA complex preceding codon recognition on the ribosome*. 1996. *J. Biol. Chem.* 271:646–52 PMID: 8557669

23. Pape T, Wintermeyer W, Rodnina MV. *Induced fit in initial selection and proofreading of aminoacyl-tRNA on the ribosome*. 1999. *EMBO J.* 18:3800–7 PMID: 10393195

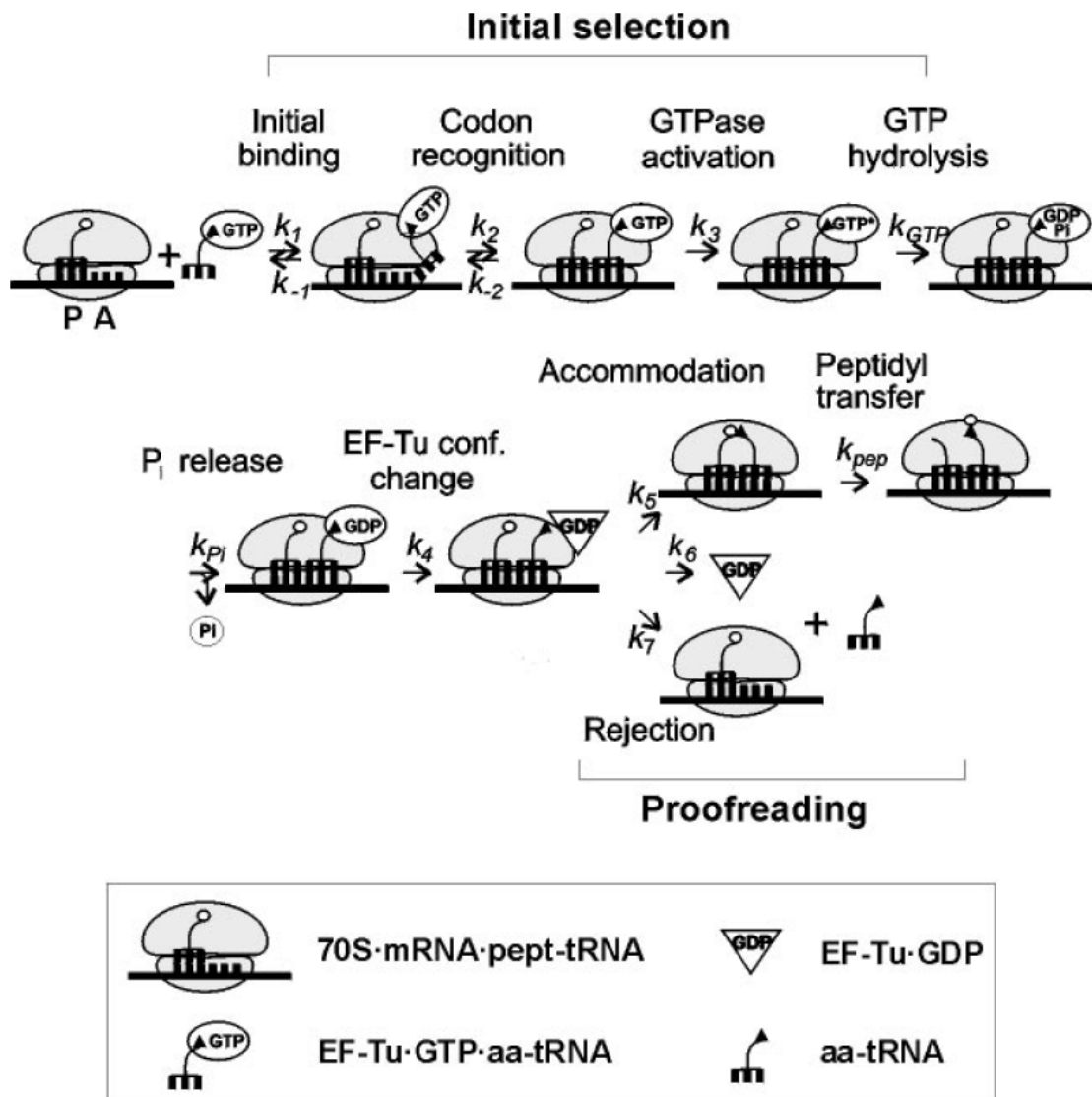


Figure 1 Kinetic scheme of aa-tRNA binding to the ribosomal A site. Measured values for the rate constants identified by numerals are summarized in Tables 1 and 4. The rates of the chemical steps are limited by the respective preceding steps. The two stages of selection are indicated. EF-Tu is depicted differently in the GTP- and GDP-bound conformations. For details, see text. Abbreviations: 70S, 70S ribosome; pept-tRNA, peptidyl-tRNA; P, peptidyl-tRNA binding site; A, aminoacyl-tRNA binding site; P_i , inorganic phosphate.